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AU 1806

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/325,278*

DATE: 10/07/96
TIME: 15:16:29

INPUT SET: S13044.raw

> This Raw Listing contains the General
> Information Section and up to the first 5 pages.

```
 1                            SEQUENCE LISTING
 2
 3    (1)    General Information:
 4
 5       (i) APPLICANT: Bj-rck, Lars
 6                      Sj-bring, Ulf
 7
 8      (ii) TITLE OF INVENTION: PROTEIN L AND HYBRID PROTEINS THEREOF
 9
10     (iii) NUMBER OF SEQUENCES: 14
11
12      (iv) CORRESPONDENCE ADDRESS:
13           (A) ADDRESSEE: SEED and BERRY LLP
14           (B) STREET: 6300 Columbia Center, 701 Fifth Avenue
15           (C) CITY: Seattle
16           (D) STATE: Washington
17           (E) COUNTRY: USA
18           (F) ZIP: 98104-7092
19
20       (v) COMPUTER READABLE FORM:
21           (A) MEDIUM TYPE: Floppy disk
22           (B) COMPUTER: IBM PC compatible
23           (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24           (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
25
26      (vi) CURRENT APPLICATION DATA:
27           (A) APPLICATION NUMBER: US 08/325,278
28           (B) FILING DATE: 26-OCT-1996
29           (C) CLASSIFICATION:
30
31    (viii) ATTORNEY/AGENT INFORMATION:
32           (A) NAME: McMasters, David D.
33           (B) REGISTRATION NUMBER: 33,963
34           (C) REFERENCE/DOCKET NUMBER: 450023.401
35
36      (ix) TELECOMMUNICATION INFORMATION:
37           (A) TELEPHONE: (206) 622-4900
38           (B) TELEFAX: (206) 682-6031
39
40
41    (2) INFORMATION FOR SEQ ID NO:1:
42
43       (i) SEQUENCE CHARACTERISTICS:
44           (A) LENGTH: 305 amino acids
45           (B) TYPE: amino acid
46           (C) STRANDEDNESS: unknown
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RAW SEQUENCE LISTING
PATENT APPLICATION   *US/08/325,278*

INPUT SET: S13044.raw

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47                (D) TOPOLOGY: unknown
48
49        (ii) MOLECULE TYPE: protein
50
51       (iii) HYPOTHETICAL: NO
52
53        (vi) ORIGINAL SOURCE:
54                (A) ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
55
56
57
58        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
59
60        Ala Val Glu Asn Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser
61        1               5                   10                  15
62
63        Glu Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser
64                    20              25                  30
65
66        Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu
67                35                  40                  45
68
69        Ala Tyr Ala Tyr Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr
70            50                  55                  60
71
72        Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
73        65                  70                  75                  80
74
75        Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
76                        85                  90                  95
77
78        Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
79                    100                 105                 110
80
81        Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu
82                115                 120                 125
83
84        Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
85            130                 135                 140
86
87        Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro
88        145                 150                 155                 160
89
90        Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys
91                    165                 170                 175
92
93        Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu
94                180                 185                 190
95
96        Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Glu Asn Gly Lys Tyr Thr
97                195                 200                 205
98
99        Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
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PATENT APPLICATION *US/08/325,278*

INPUT SET: S13044.raw

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101
102      Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
103      225             230                 235                 240
104
105      Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
106                      245                 250                 255
107
108      Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
109                  260                 265                 270
110
111      Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr
112              275                 280                 285
113
114      Thr Ile Asn Ile Arg Phe Ala Gly Lys Lys Val Asp Glu Lys Pro Glu
115          290                 295                 300
116
117      Glu
118      305
119
120  (2) INFORMATION FOR SEQ ID NO:2:
121
122      (i) SEQUENCE CHARACTERISTICS:
123          (A) LENGTH: 921 base pairs
124          (B) TYPE: nucleic acid
125          (C) STRANDEDNESS: double
126          (D) TOPOLOGY: unknown
127
128     (ii) MOLECULE TYPE: DNA (genomic)
129
130    (iii) HYPOTHETICAL: NO
131
132     (vi) ORIGINAL SOURCE:
133          (A) ORGANISM: Escherichia coli LE392/pHDL, DSM 7054
134
135
136
137     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
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139  GCGGTAGAAA ATAAAGAAGA AACACCAGAA ACACCAGAAA CTGATTCAGA AGAAGAAGTA        60
140
141  ACAATCAAAG CTAACCTAAT CTTTGCAAAT GGAAGCACAC AAACTGCAGA ATTCAAAGGA       120
142
143  ACATTTGAAA AAGCAACATC AGAAGCTTAT GCGTATGCAG ATACTTTGAA GAAAGACAAT       180
144
145  GGAGAATATA CTGTAGATGT TGCAGATAAA GGTTATACTT TAAATATTAA ATTTGCTGGA       240
146
147  AAAGAAAAAA CACCAGAAGA ACCAAAAGAA GAAGTTACTA TTAAAGCAAA CTTAATCTAT       300
148
149  GCAGATGGAA AAACACAAAC AGCAGAATTC AAAGGAACAT TTGAAGAAGC AACAGCAGAA       360
150
151  GCATACAGAT ATGCAGATGC ATTAAAGAAG GACAATGGAG AATATACAGT AGACGTTGCA       420
152
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INPUT SET: S13044.raw

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153   GATAAAGGTT ATACTTTAAA TATTAAATTT GCTGGAAAAG AAAAAACACC AGAAGAACCA      480
154
155   AAAGAAGAAG TTACTATTAA AGCAAACTTA ATCTATGCAG ATGGAAAAAC ACAAACAGCA      540
156
157   GAATTCAAAG GAACATTTGA AGAAGCAACA GCAGAAGCAT ACAGATATGC TGACTTATTA      600
158
159   GCAAAAGAAA ATGGTAAATA TACAGTAGAC GTTGCAGATA AAGGTTATAC TTTAAATATT      660
160
161   AAATTTGCTG GAAAAGAAAA AACACCAGAA GAACCAAAAG AAGAAGTTAC TATTAAAGCA      720
162
163   AACTTAATCT ATGCAGATGG AAAAACTCAA ACAGCAGAGT TCAAAGGAAC ATTTGCAGAA      780
164
165   GCAACAGCAG AAGCATACAG ATACGCTGAC TTATTAGCAA AAGAAAATGG TAAATATACA      840
166
167   GCAGACTTAG AAGATGGTGG ATACACTATT AATATTAGAT TTGCAGGTAA GAAAGTTGAC      900
168
169   GAAAAACCAG AAGAATAATA A                                                921
170
171   (2) INFORMATION FOR SEQ ID NO:3:
172
173       (i) SEQUENCE CHARACTERISTICS:
174           (A) LENGTH: 434 amino acids
175           (B) TYPE: amino acid
176           (C) STRANDEDNESS: unknown
177           (D) TOPOLOGY: unknown
178
179      (ii) MOLECULE TYPE: protein
180
181     (iii) HYPOTHETICAL: NO
182
183      (vi) ORIGINAL SOURCE:
184           (A) ORGANISM: Escherichia coli LE392/pHDLG, DSM 7055
185
186
187
188      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
189
190      Ala Val Glu Asn Lys Glu Glu Thr Pro Glu Thr Pro Glu Thr Asp Ser
191      1               5                   10                  15
192
193      Glu Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Phe Ala Asn Gly Ser
194                  20                  25                  30
195
196      Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Lys Ala Thr Ser Glu
197              35                  40                  45
198
199      Ala Tyr Ala Tyr Ala Asp Thr Leu Lys Lys Asp Asn Gly Glu Tyr Thr
200          50                  55                  60
201
202      Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
203      65                  70                  75                  80
204
205      Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
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206                          85                        90                        95
207
208    Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
209                100                   105                   110
210
211    Thr Phe Glu Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Ala Leu
212            115                   120                   125
213
214    Lys Lys Asp Asn Gly Glu Tyr Thr Val Asp Val Ala Asp Lys Gly Tyr
215        130                   135                   140
216
217    Thr Leu Asn Ile Lys Phe Ala Gly Lys Glu Lys Thr Pro Glu Glu Pro
218    145                   150                   155                   160
219
220    Lys Glu Glu Val Thr Ile Lys Ala Asn Leu Ile Tyr Ala Asp Gly Lys
221                165                   170                   175
222
223    Thr Gln Thr Ala Glu Phe Lys Gly Thr Phe Glu Glu Ala Thr Ala Glu
224                180                   185                   190
225
226    Ala Tyr Arg Tyr Ala Asp Leu Leu Ala Lys Glu Asn Gly Lys Tyr Thr
227                195                   200                   205
228
229    Val Asp Val Ala Asp Lys Gly Tyr Thr Leu Asn Ile Lys Phe Ala Gly
230        210                   215                   220
231
232    Lys Glu Lys Thr Pro Glu Glu Pro Lys Glu Glu Val Thr Ile Lys Ala
233    225                   230                   235                   240
234
235    Asn Leu Ile Tyr Ala Asp Gly Lys Thr Gln Thr Ala Glu Phe Lys Gly
236                245                   250                   255
237
238    Thr Phe Ala Glu Ala Thr Ala Glu Ala Tyr Arg Tyr Ala Asp Leu Leu
239            260                   265                   270
240
241    Ala Lys Glu Asn Gly Lys Tyr Thr Ala Asp Leu Glu Asp Gly Gly Tyr
242        275                   280                   285
243
244    Thr Ile Asn Ile Arg Phe Ala Gly Lys Lys Val Asp Glu Lys Pro Glu
245        290                   295                   300
246
247    Glu Pro Met Asp Thr Tyr Lys Leu Ile Leu Asn Gly Lys Thr Leu Lys
248    305                   310                   315                   320
249
250    Gly Glu Thr Thr Thr Glu Ala Val Asp Ala Ala Thr Ala Glu Lys Val
251                325                   330                   335
252
253    Phe Lys Gln Tyr Ala Asn Asp Asn Gly Val Asp Gly Glu Trp Thr Tyr
254                340                   345                   350
255
256    Asp Asp Ala Thr Lys Thr Phe Thr Val Thr Glu Lys Pro Glu Val Ile
257                355                   360                   365
258
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